

WEST**Help****Logout****Interrupt****Main Menu****Search Form****Posting Counts****Show S Numbers****Edit S Numbers****Preferences****Search Results -****Terms****Documents**

13 same (conjugat\$ or fuse\$)

10

Database:

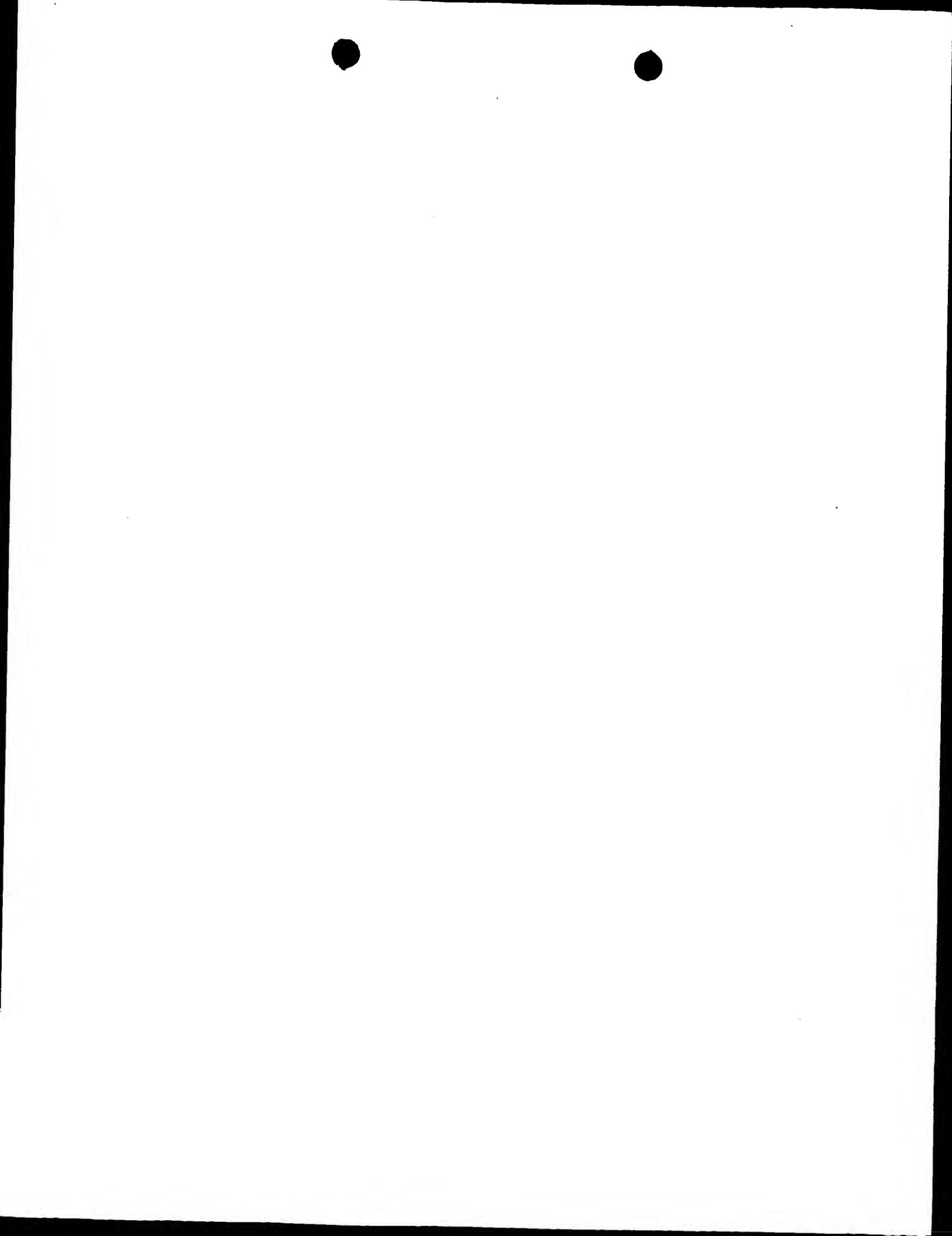
US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

13 same (conjugat\$ or fuse\$)

Refine Search:**Clear****Search History****Today's Date: 1/17/2002**

DB Name	Query	Hit Count	Set Name
USPT	13 same (conjugat\$ or fuse\$)	10	L4
USPT	12 same peptide\$	66	L3
USPT	albumin\$ same composition\$ same (stability or stable)	548	L2
USPT	fusion adj (protein\$ or polypeptide\$ or polyprotein\$)	12092	L1

09/424,080



(FILE 'HOME' ENTERED AT 12:50:47 ON 17 JAN 2002)

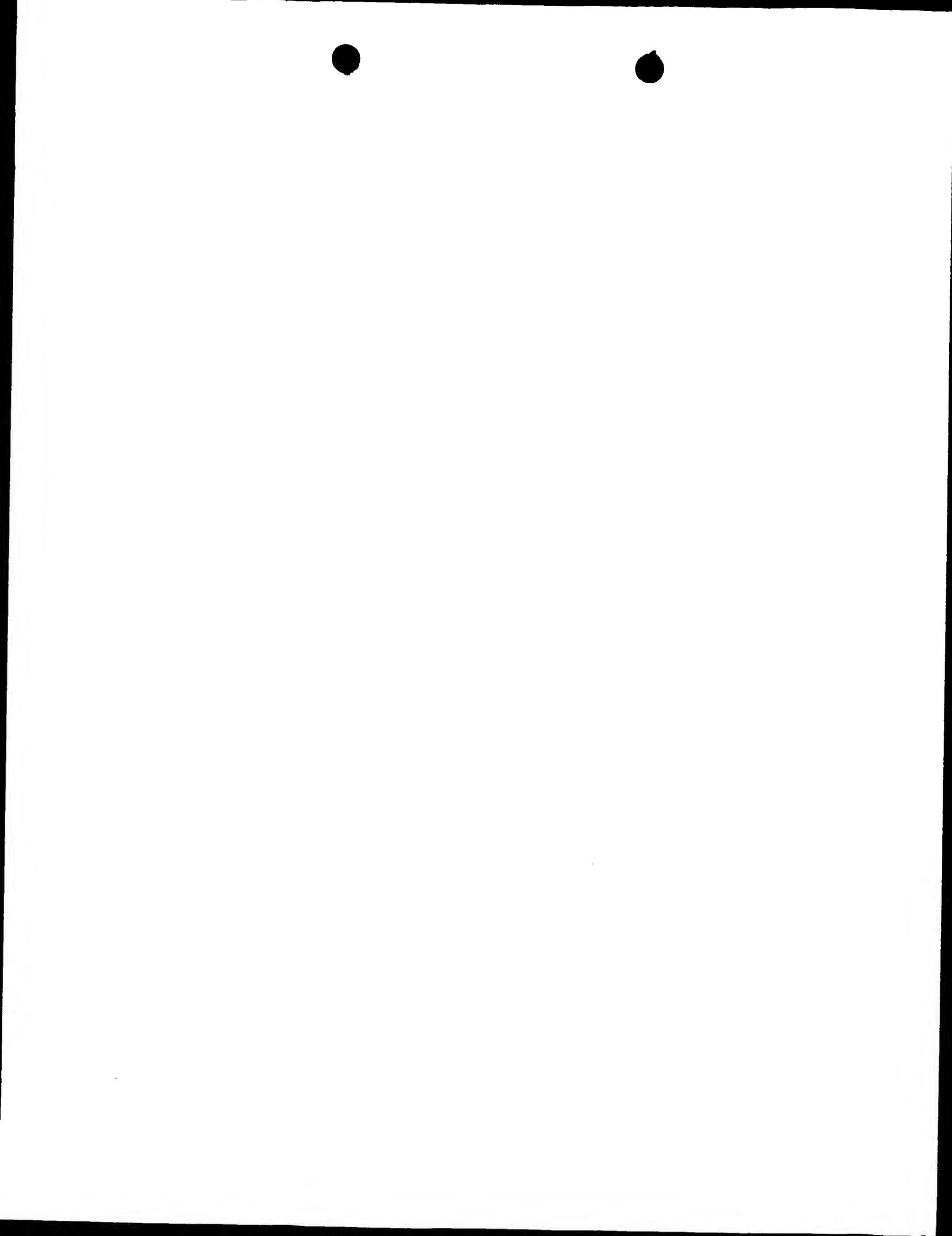
FILE 'MEDLINE' ENTERED AT 12:50:55 ON 17 JAN 2002

L1 128 S ALBUMIN (P) (STABILITY OR STABLE) (P) PEPTIDE?
L2 20 S L1 AND (FUSION? OR CONJUGATE?)
L3 20 DUP REM L2 (0 DUPLICATES REMOVED)

=>

09|424,080

1|17|02.



=> d his

(FILE 'HOME' ENTERED AT 13:45:18 ON 17 JAN 2002)
SET COST OFF

FILE 'REGISTRY' ENTERED AT 13:45:27 ON 17 JAN 2002
L1 138 S LTEKKYSP/SQSP
L2 1 S L1 AND 8/SQL

FILE 'HCAOLD' ENTERED AT 13:45:45 ON 17 JAN 2002
L3 0 S L2

FILE 'HCAPLUS' ENTERED AT 13:45:48 ON 17 JAN 2002
L4 1 S L2

FILE 'USPATFULL, USPAT2' ENTERED AT 13:46:04 ON 17 JAN 2002
L5 0 S L2

=> fil reg
FILE 'REGISTRY' ENTERED AT 13:46:19 ON 17 JAN 2002
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STRUCTURE FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9
DICTIONARY FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d 12 sqide can

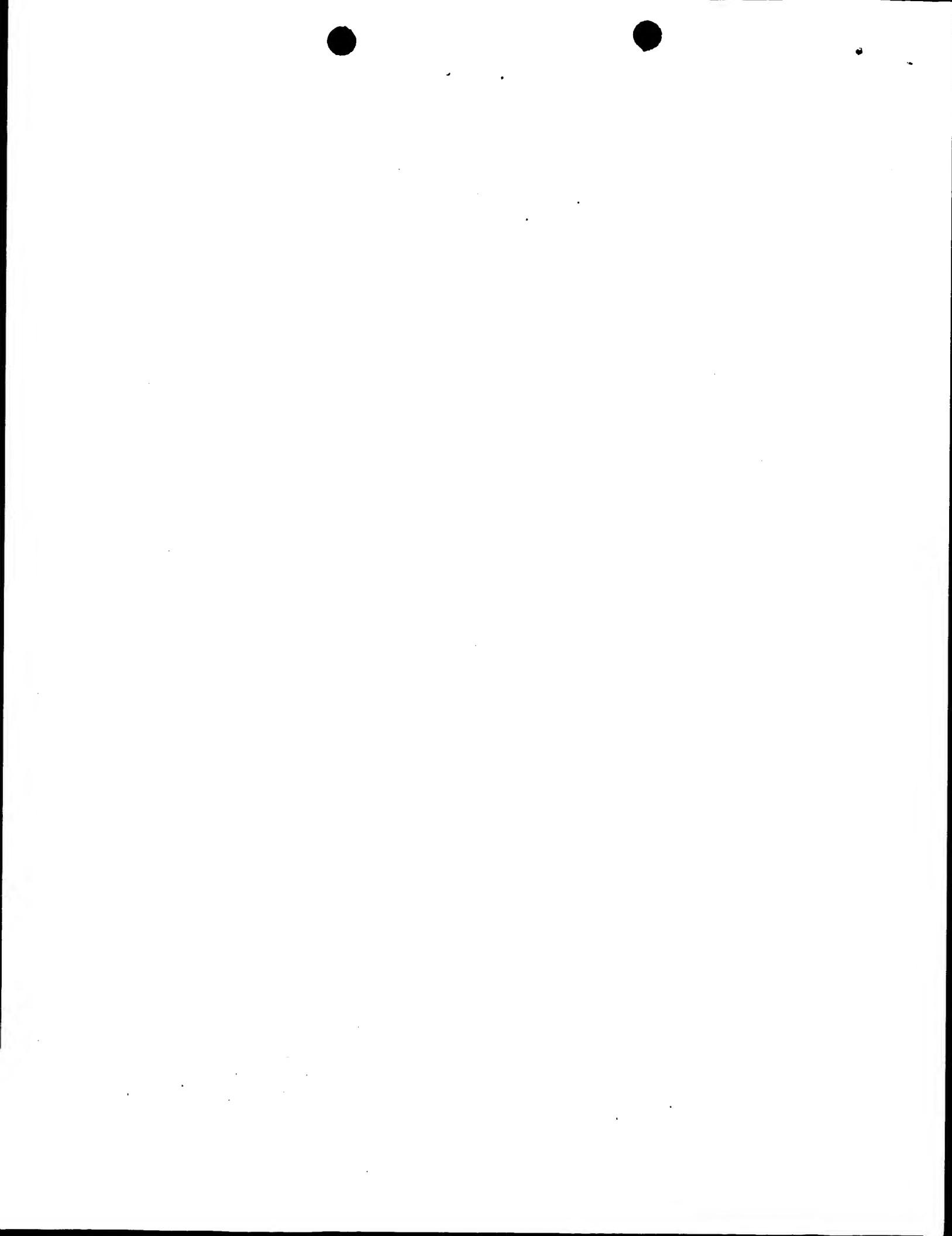
L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS
RN 216579-39-4 REGISTRY
CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-
tyrosyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 8

SEQ 1 LTEKKYSP
=====

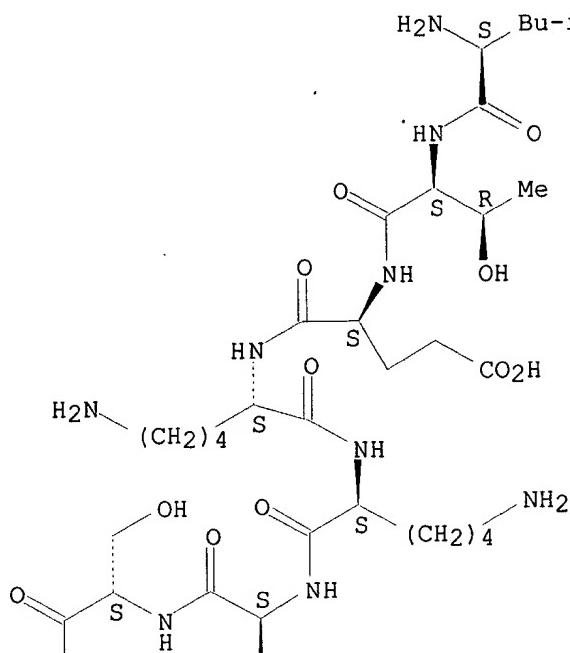
HITS AT: 1-8
MF C44 H72 N10 O14
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, TOXLIT

Absolute stereochemistry.

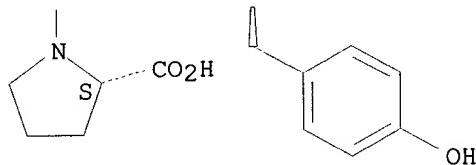
Jan Delaval
Reference Librarian
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PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

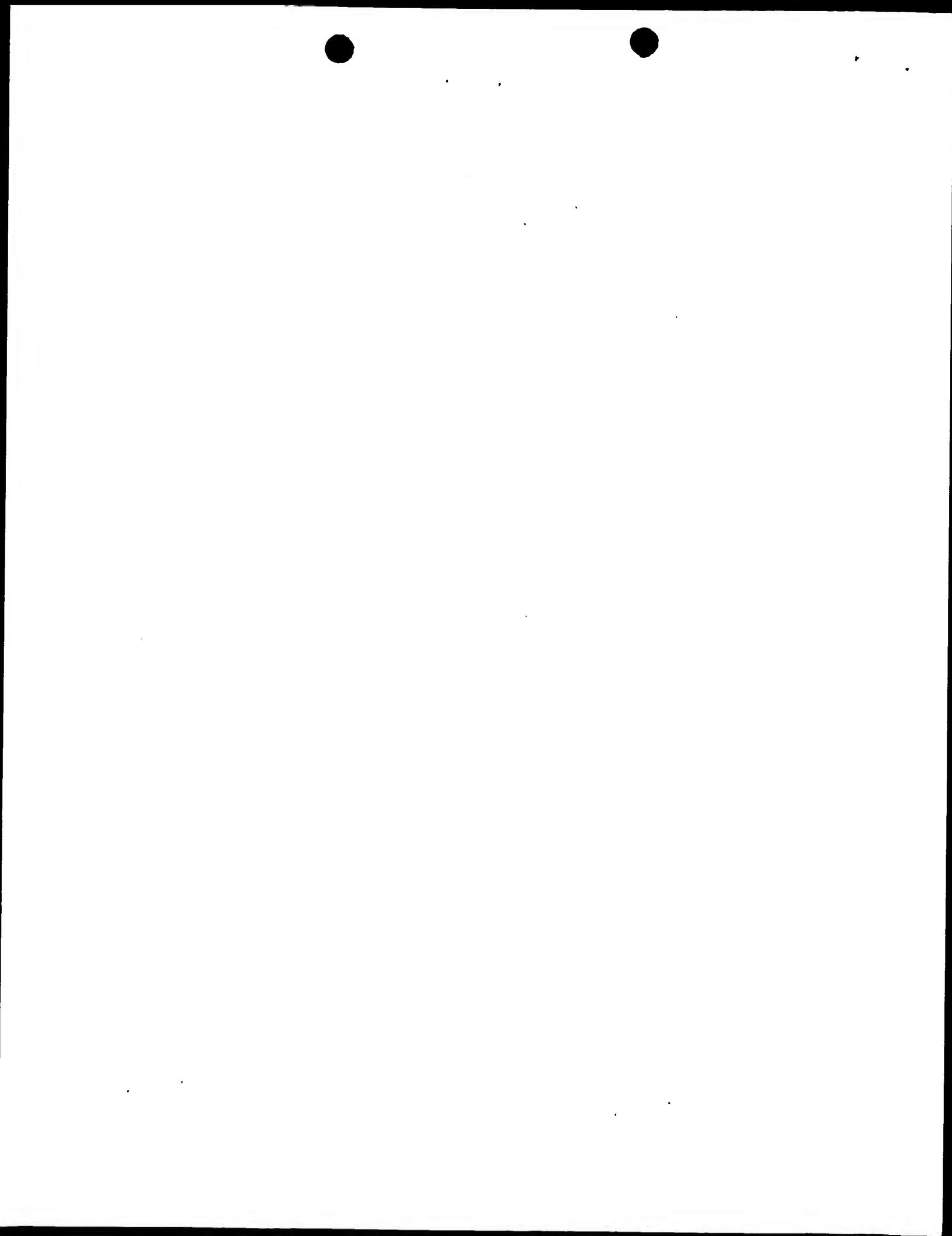
=> fil hcaplus
 FILE 'HCAPLUS' ENTERED AT 13:46:26 ON 17 JAN 2002
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FILE COVERS 1907 - 17 Jan 2002 VOL 136 ISS 3
 FILE LAST UPDATED: 16 Jan 2002 (20020116/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of



all substance data from the REGISTRY file. Enter HELP FIRST for more information.

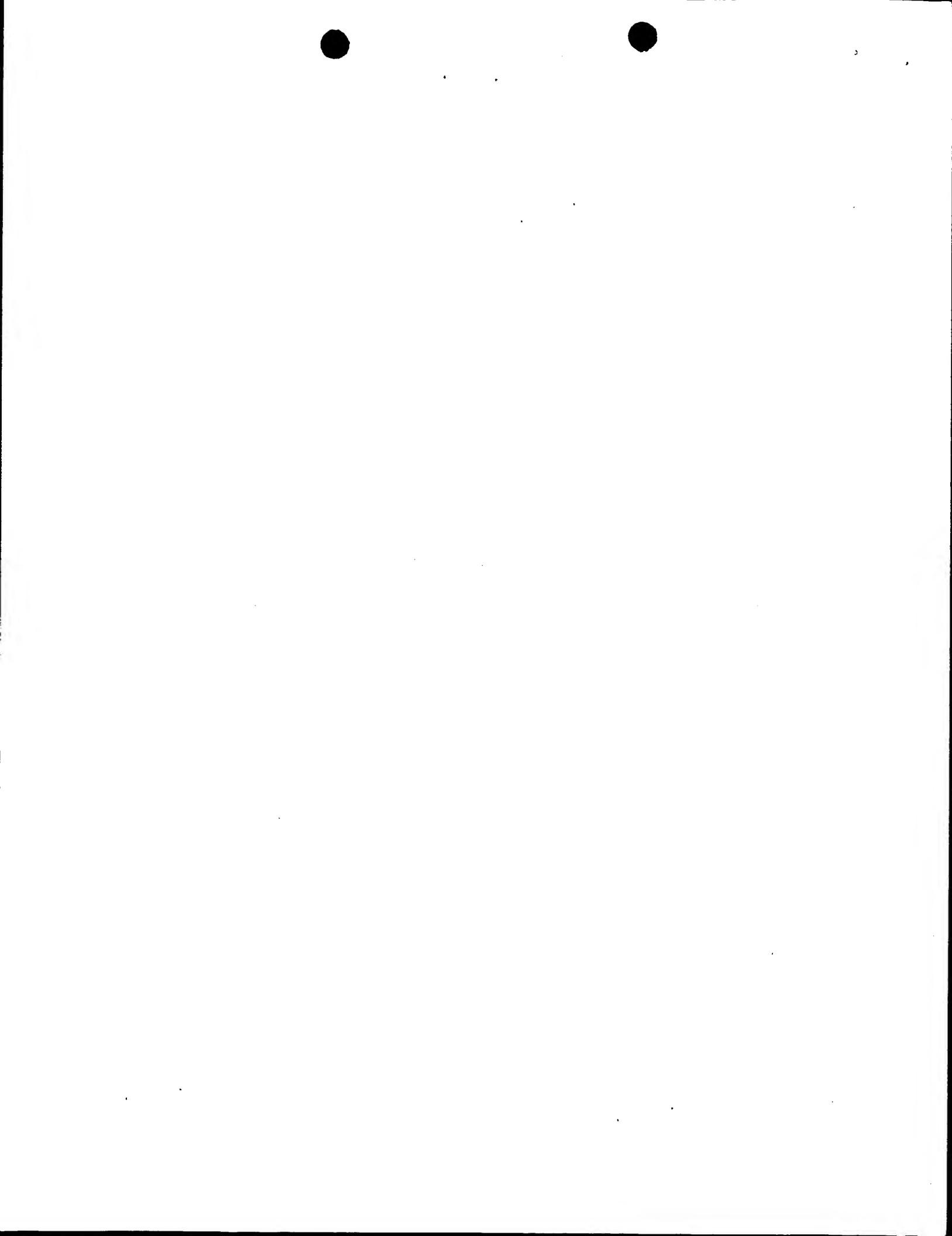
HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d 14 all

L4 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
 AN 1998:789037 HCAPLUS
 DN 130:33014
 TI Compositions for enhancing immunosuppressants pharmaceutical activities
 IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi
 PA Russia
 SO PCT Int. Appl., 26 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM A61K038-04
 ICS A61K038-13; A61K038-21
 CC 1-7 (Pharmacology)
 Section cross-reference(s): 15

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9852594	A1	19981126	WO 1998-FI418	19980518
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	FI 9702121	A	19981120	FI 1997-2121	19970519
	AU 9874352	A1	19981211	AU 1998-74352	19980518
	EP 981359	A1	20000301	EP 1998-921528	19980518
	R: AT, DE, ES, FR, GB, IT, SE, FI				
	JP 2001526675	T2	20011218	JP 1998-550009	19980518
PRAI	FI 1997-2121	A	19970519		
	WO 1998-FI418	W	19980518		
AB	The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.				
ST	immunosuppressant adjuvant formulation peptide				
IT	Interferon .tau.				
	Interferon .alpha.				
	Interferon .beta.				
RL:	PRP (Properties)				
	(antilymphoproliferative site of; compns. for enhancing				



immunosuppressant pharmaceutical activities)

IT Adenocarcinoma inhibitors
Anti-inflammatory drugs
Antirheumatic drugs
Autoimmune diseases
Drug bioavailability
Immunosuppressants
Leukemia inhibitors
Lupus erythematosus
Lymphoma inhibitors
Myasthenia gravis
Psoriasis
Transplant (organ)
Uveitis
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Interferon .alpha.2
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT Peptides, biological studies
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

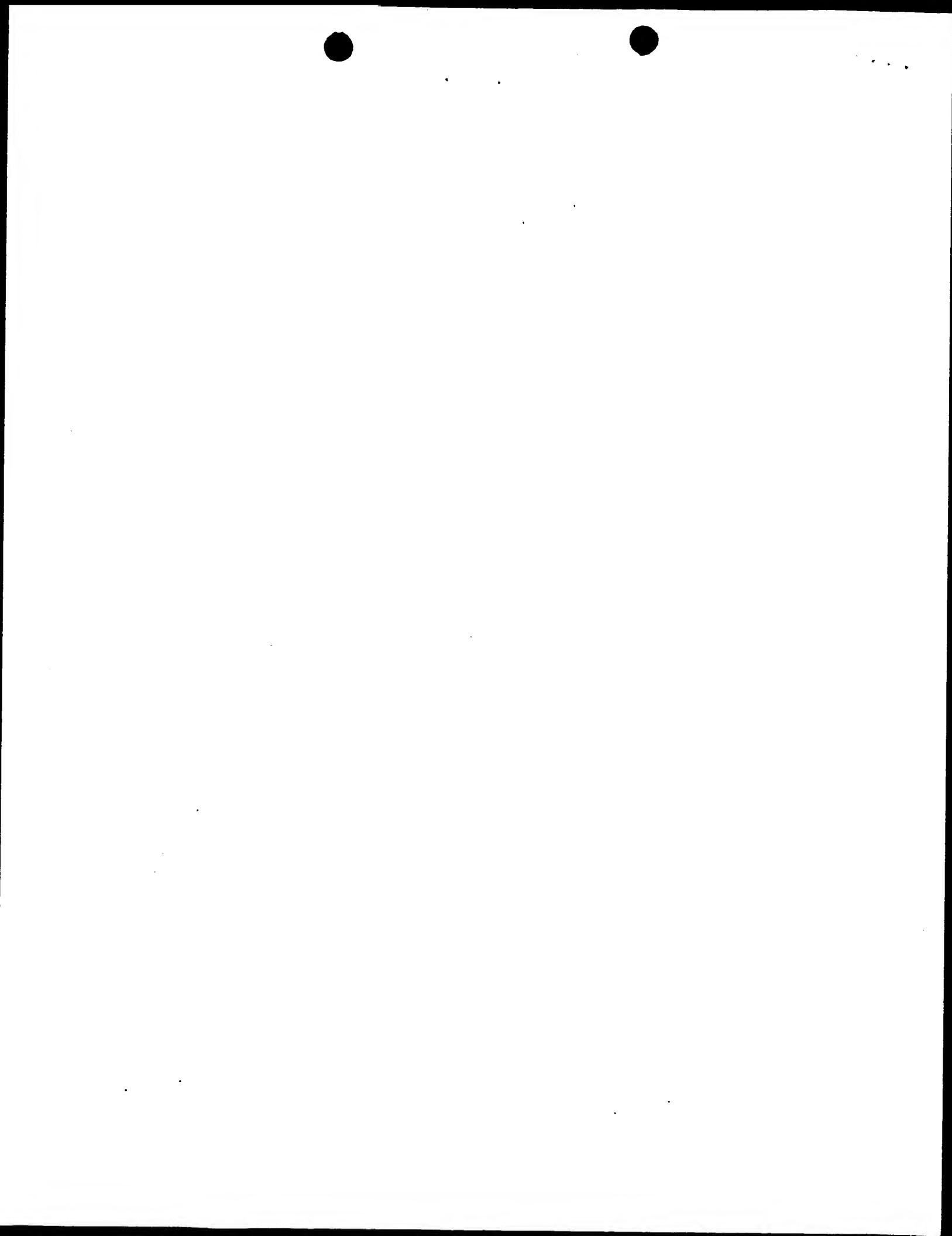
IT Interferons
RL: PRP (Properties)
(interferon .omega., antilymphoproliferative site of; compns. for enhancing immunosuppressant pharmaceutical activities)

IT Antitumor agents
(myeloma; compns. for enhancing immunosuppressant pharmaceutical activities)

IT 216579-39-4D, analogs 216579-44-1D, analogs
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(compns. for enhancing immunosuppressant pharmaceutical activities)

IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(compns. for enhancing immunosuppressant pharmaceutical activities)

RE.CNT 5
RE
(1) University of Florida; WO 9009806 A2 1990 HCPLUS
(2) University of Florida; WO 9410313 A2 1994 HCPLUS
(3) Vacsyn, S; FR 2706772 A1 1994 HCPLUS
(4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE
(5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCPLUS



Run on: January 17, 2002, 12:14:35 ; Search time 12.72 Seconds
 (without alignments)
 (47.909 Million cell updates/sec)

OM protein - protein search, using sw model

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GenCore version 4.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	21	50	0	S21663	
2	18	42	9	S11556	neuropeptide - flower beetle (Pachnoda marginata)
3	18	42	9	S15422	C;Species: Pachnoda marginata
4	18	42	9	A58641	C;Accession: S21663
5	17	40	5	A05169	C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
6	16	38	1	G37196	R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
7	16	38	1	S20162	Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
8	16	38	1	A14683	A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va
9	16	38	1	S21663	etrometry.
10	16	38	1	A5651	A;Reference number: S21663; MUID:92265187
11	14	33	3	1 HOROHA	A;Accession: S21663
12	14	33	3	A04111	A;Status: preliminary
13	14	33	3	P0087	A;Molecule type: Protein
14	14	33	3	S0027	A;Residues: 1-8 <GAE>
15	14	33	3	P0029	C;Keywords: oxidoreductase
16	14	33	3	A61348	Query Match 42.9%; Score 18; DB 2; Length 6;
17	14	33	3	S08995	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
18	14	33	3	A49823	Query Match 42.9%; Score 18; DB 2; Length 6;
19	14	33	3	A44960	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
20	14	33	3	A43976	Query Match 42.9%; Score 18; DB 2; Length 6;
21	14	33	3	B43976	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
22	14	33	3	S11545	Query Match 42.9%; Score 18; DB 2; Length 6;
23	14	33	3	D47393	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
24	13	31	0	P00150	Query Match 42.9%; Score 18; DB 2; Length 6;
25	12	28	6	P00689	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
26	12	28	6	S11976	Query Match 42.9%; Score 18; DB 2; Length 6;
27	12	28	6	S16324	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
28	12	28	6	A23967	Query Match 42.9%; Score 18; DB 2; Length 6;
29	11	26	2	E44823	Best Local Similarity 75.0%; Pred. No. 2.2e+05; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Major protein anti-copper resistance T-cell receptor beta amelotin - rat mosquitoicidal toxin contraction-inhibitor T-cell receptor beta T-cell receptor be laminin B1 - westie fatty-acid syntaxis Ig kappa chain V-I aggrecan - bovine DNA topoisomerase T-cell receptor beta virotoxin - destro hypertrehalosemic

RESULT 3
S15422 adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Geede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-peptide
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (NRP) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YSP 8
Db 4 YSP 6

RESULT 4
A5841 adipokinetic hormone - dor beetle
C;Species: Goetrus stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A5841
R;Geede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-peptide
A;Reference number: S15422; MUID:91248100
A;Accession: A5841
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (NRP) #status experimental

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YSP 8
Db 4 YSP 6

RESULT 5
A05169 neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Accession: A05169
R;Witten, J.L.; Schaffner, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A;Reference number: A90118; MUID:85046530
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

Query Match 38.1%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 EKKY 6
Db 2 EKDY 5

RESULT 6
G37196 bradykinin-potentiating Peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptide
A;Reference number: A37196; MUID:90351557
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 38.1%; Score 16; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKYS 8
Db 1 QKWP 5

RESULT 7
B44510 hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C;Species: Lactococcus lactis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: B44510
R;Renault, P.; Gaillardin, C.; Heslot, H.
J. Bacteriol. 171, 3108-3114, 1989
A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation
A;Reference number: A44510; MUID:89255069
A;Accession: B44510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <REN>
A;Cross-references: EMBL:M90762

Query Match 38.1%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

us-09-424-080a-1.closed.Esp

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GenCore version 4.5

Run on: January 17, 2002, 12:15:20 ; Search time 10.03 Seconds
 (without alignments)
 29.244 Million cell updates/sec

OM protein - protein search, using sw model

Title: US-09-424-080A-1
Perfect score: 42
Sequence: I LTERKYSVP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36564827 residues

Actual number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: SwissProt_39,*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	19	45.2	8	1 UH09_RAT	P56575 rattus norv
2	18	42.9	8	1 AKL_MEMLM	P25423 melolontha
3	16	38.1	5	1 BPP1_BOVIN	P30425 bothrops in
4	14	33.3	5	1 PRCT_PERAM	P01373 periplaneta
5	14	33.3	6	1 ASP2_LACGS	P82655 lactobacilli
6	14	33.3	6	1 OVM_LDEPDN	P42985 leptinotars
7	14	33.3	8	1 ALL4_CALVO	P41840 calliphora
8	14	33.3	8	1 HTF1_PERAM	P04540 periplaneta
9	14	33.3	8	1 HTF_TENMO	P25419 tenebrio mo
10	14	33.3	8	1 RPCH_PANBO	P08939 panulus bo
11	13	31.0	7	1 LMT2_LOCMI	P22396 locusta mig
12	12	28.6	8	1 FARS_HIRME	P42565 hirudo medi
13	12	28.6	8	1 AL17_CARMA	P811820 carinurus ma
14	12	28.6	8	1 ALL3_CYDPO	P02155 cydla ponon
15	12	28.6	8	1 ALL4_CYDPO	P813049 leucophaea
16	12	28.6	8	1 LPK_LCEUMA	P81817 carcinus ma
17	11	26.2	5	1 AL14_CARMA	P31736 mytilus edu
18	11	26.2	6	1 CIP1_WNTED	P23210 herpes simp
19	11	26.2	7	1 VP19_HSVIK	P82158 cydla ponon
20	11	26.2	7	1 AL17_CYDPO	P25418 libellula a
21	11	26.2	8	1 AKH_LIBAU	P14595 tabanus atr
22	11	26.2	8	1 ARH_TABAT	P81819 carcinus ma
23	11	26.2	8	1 AL15_CARMA	P81820 carcinus ma
24	11	26.2	8	1 AL16_CARMA	P81821 carcinus ma
25	11	26.2	8	1 AL18_CARMA	P82152 cydla ponon
26	11	26.2	8	1 ALL1_CYDPO	P81809 carcinus ma
27	11	26.2	8	1 ALL7_CARMA	P81809 carcinus ma
28	11	26.2	8	1 HTP2_PERAM	P19990 periplaneta
29	11	26.2	8	1 ICK8_LFUMA	P82692 periplaneta
30	11	26.2	8	1 PPK2_PERAM	P05294 dactylylum d
31	10	23.8	7	1 IGAO_MACDE	P41487 homarus ame
32	10	23.8	8	1 RFA_HOMAM	NPB_BOVIN
33	10	23.8	8	1 NPB_BOVIN	P15507 bos taurus

ALIGNMENTS

RESULT	1	UH09_RAT	STANDARD:	PRT:	8 AA.
ID	UH09_RAT				
AC	P56575;	Query Match	45.2%	score 19;	DB 1; Length 8;
DT	15-DEC-1998	Best Local Similarity	50.0%	pred. No. 1e+05;	
DT	15-DEC-1998 (Rel. 37, last sequence update)	Mismatches	2;		
DT	15-DEC-1998 (Rel. 37, last annotation update)	Indels	0;		
DE	UNKNOWN PROTEIN FROM 2D PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).	Gaps	0;		
OS	Rattus norvegicus (Rat);				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=WISTAR; TISSUE=Heart;				
RA	LA X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salnikov J.,				
RL	Jungblut P. R.;				
CC	Submitted (SEP-1998) to the SWISS-PROT data bank.				
CC	-1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 8.9. ITS MW IS: 42 KDA.				
FT	NON_TER				
SQ	SEQUENCE	8 AA;	1029 MW;	9E0775A6C4140B06 CRC64;	
RESULT	2				
AKR_MEMLM	Query Match	45.2%	score 19;	DB 1; Length 8;	
TD	AKR_MEMLM	Best Local Similarity	50.0%	pred. No. 1e+05;	
AC	P25423;	Mismatches	2;		
DT	01-MAY-1992 (Rel. 22, created)	Indels	0;		
DT	01-FEB-1994 (Rel. 28, last sequence update)	Gaps	0;		
DE	01-FEB-1994 (Rel. 28, last annotation update)				
ADIPOKINETIC HORMONE (AKH)	DT				
Melolontha melolontha (Cockchafer),	DE				
OS	Geotrupes stercorosus (Dor beetle), and				
OS	Pachynota marginata (Flower beetle), and				
OC	Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;				
OC	Sarabaeidae; Scarabaeidae; Melolonthinae; Melolontha;				
OX	NCBI_TaxID=7061, 7087, 7058;				
RN	[1]				
RP	SEQUENCE.				
RC	SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;				
RX	MEDLINE=91248100; PubMed=2039445;				
RA	Grede G.;				
RT	A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating peptide family isolated and sequenced from two beetle species.;				

RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1580453;
 RA Gaede G., Lopata A., Kellner R., Rinchart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 cardiaca of various cetonid beetle species determined by
 pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 spectrometry";
 RT Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -I- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR: S15422; S15422.
 PIR: S21663; S21663.
 DR Interpro: IPR002047; AKH.
 KW Peptidergic system; Insecta; Arthropoda; Hexapoda; Insecta;
 DR Interpro: IPR002047; AKH.
 FT MOD_RES: 1 1 AMIDATION; Flight.
 FT MOD_RES: 8 8 AMIDATION CARBOXYLIC ACID.
 SQ SEQUENCE: 8 AA; 1022 MW; 867AB775AB54736 CRC64;

Query Match
 Best Local Similarity 42.9%; Score 18; DB 1; Length 8;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YSP 8
 Db . 4 YSP 6

RESULT 3

BP7_BOTIN STANDARD: PRT; 5 AA.

ID , BP7_BOTIN STANDARD: PRT; 5 AA.
 AC P30425;
 DT 01-FEB-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DT 01-FEB-1994 (Rel. 28, last annotation update)
 DE BRADYKININ-POTENTIATING PEPTIDE S5, 2 (5A) (ANGIOTENSIN-CONVERTING
 ENZYME INHIBITOR).
 OS Bothrops insularis (Island jararaca) (Queimada Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 NJ NCBI_TaxID=8723;
 RN [1]
 SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.";
 RL Protein Chem. 9:221-227(1990).
 CC -I- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF THE
 BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: G37196; G37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES: 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE: 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match
 Best Local Similarity 38.1%; Score 16; DB 1; Length 5;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRYSP 8
 :|:|:
 RESULT 5
 ID ASP2_LACSN STANDARD: PRT; 6 AA.

Db 1 OKWAP 5

RESULT 4
 ID PRCT_PERAM STANDARD: PRT; 5 AA.
 AC PRCT_PERAM
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1985 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PROCTOLIN.
 RX NOCB_TaxID=6978, 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=6074708; PubMed=576;
 RA Starrett A.N., Brown B.B.;
 RT in insects.";
 RL Life Sci. 17:1253-1256(1975).
 [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=8122865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron."
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polypheus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrov A.'
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shababowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 horseshoe crab Limulus polyphemus";
 RL peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=8632783; PubMed=2872661;
 RA Stangler J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, *Carcinus maenas*.";
 RL Peptides 7:67-72(1986).
 CC -I- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -I- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR: A01644; HOROHA.
 DR PIR: A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE: 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match
 Best Local Similarity 50.0%; Score 14; DB 1; Length 5;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KYSP 8
 :|:|:
 DB 1 RYLP 4

RESULT 5
 ID ASP2_LACSN STANDARD: PRT; 6 AA.

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Gencore version 4.5

OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:50 ; Search time 22.03 Seconds
 (without alignments)
 53.118 Million cell updates/sec

Title:	US-09-424-080A-1				
perfect score:	42				
Sequence:	1 LTEKKYSP 8				
scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext 0.5				
Searched:	473505 seqs, 146272329 residues				
Minimum DB seq length:	0				
Maximum DB seq length:	8				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
database :	<ul style="list-style-type: none"> - SPTRREMBL_17:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rabbit:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 				
pred. No.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
Result No.	Score	Query	Match Length	DB ID	Description
1	25	59.5	8	2 Q9R9E0	Q9r9e0 badillius su P82101 litoria rub
2	14	33.3	7	13 P82101	Q9tmn4 begonia for P82101 litoria rub
3	14	33.3	8	8 Q9T2Y3	Q9tmn4 begonia for Q9t2y2 begonia tai
4	14	33.3	8	9 Q9T2Y2	Q9t2y2 begonia apt
5	14	33.3	8	9 Q9T2Y1	Q9t2y1 begonia apt
6	14	33.3	10	9 Q9XGL9	Q9xgl9 begonia chi
7	14	33.3	8	10 Q9XGL8	Q9xgl9 begonia chi Q9xgl8 begonia pal
8	14	33.3	10	9 Q9STD5	Q9std5 begonia pal Q9rtz2 escherichia
9	13	31.0	10	2 Q9RTZ2	Q9rtz2 escherichia
10	13	31.0	8	12 Q84271	Q84271 human papil
11	12	28.6	8	6 Q9XSY1	Q9xsy1 canis famili
12	12	28.6	8	8 Q35792	Q35792 saccharomyces cerevisiae
13	12	28.6	8	11 Q62933	Q62933 rattus norvegicus
14	11	26.2	7	2 Q54248	Q54248 streptomyces
15	11	26.2	8	2 Q56429	Q56429 thermus aquo
16	11	26.2	8	2 Q8R517	Q8r517 clostridium
17	11	26.2	8	4 Q15895	Q15895 homo sapien
18	11	26.2	8	5 P82689	P82689 periplaneta americana
19	11	26.2	8	8 P82929	P82929 bos taurus

RESULTS

RESULT	1	PRELIMINARY;	PRT;	8 AA.
Q9R9E0	Q9R9E0			
ID	Q9R9E0;			
AC	Q9R9E0;			
DT	01-MAY-2000 (TREMBLEL 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLEL 13, Last annotation update)			
DE	STAGE V SPORULATION PROTEIN E (FRAGMENT).			
GN	SPOVE.			
OS	Bacillus subtilis.			
OC	Bacillales; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/staphylococcus group; Bacillus.			
OX	NCBL_TAXID=123;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=68;			
RX	MEDLINE=93003529; PubMed=1391053;			
RA	Henriques A.O., de Lencastre H., Pigott P.J.;			
RT	"A Bacillus subtilis morphoene cluster that includes homologous to the mra region of Escherichia coli.";			
RT	Biochimie 74:735-748(1993).			
RL				
DR	EMBL; X64258; CAA45561.1; -.			
FT	NON_TER 8 AA; 893 MW; EEE75A1A33321B1A6 CRC64;			
SQ	SEQUENCE 8 AA; 893 MW;			

RESULTS

RESULT	2	PRELIMINARY;	PRT;	7 AA.
P82101	P82101			
ID	P82101;			
AC	P82101;			
DT	01-MAY-2000 (TREMBLEL 13, Cocrated)			
DT	01-MAY-2000 (TREMBLEL 13, Last sequence update)			
DT	01-MAY-2000 (TREMBLEL 13, Last annotation update)			

ALIGNMENTS

DE
 OS
 OC
 OC
 OC
 OC
 OX
 RN
 RP
 SBQSEQUENCE.
 RC
 TISSUE=SKIN SECRETION;
 RA
 Rabbit P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT
 "Peptides from the skin glands of the Australian buzzing tree frog
 litoria electrica. Comparison with the skin peptides from Litoria
 rubella.",
 RL
 Aust. J. Chem. 52:0-0(1999).
 KW
 Amphibian skin; Amidation.
 FT
 MOD_RES 7 AMIDATION.
 SEQUENCE 7 AA; 834 MW; 6DDDB5B076B0B5030 CRC64:
 SQ

te; Tracheophyta; eudicots; Rosidae;

OS	DE
OC	Litoria rubella (Desert tree frog)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC	Litoria.
OX	NCBI_TaxID=104895;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=SKIN SECRETION;
RA	Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT	"Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella.,"
RL	Aust. J. Chem. 52:0-0(1999).
KW	Amphibian skin; Amidation.
FT	MOD_RES 7 7 AMIDATION.
SQ	SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

te; Tracheophyta;
eudicots; Rosidae;

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Query Match          33.3%; Score 14; DB 13; Length 7;
Best Local Similarity 66.7%; pred. No. 4.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;
QY      6 YSP 8
       | |
Db      2 YEP 4

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	Best	Local	Similarity	8	
Matches	3;	Conservative	75.0%	Pred. No. 4.7e+05;	1;
QY	2	TEKK	5	Mismatches	
Db	5	TEPK	8		

9th 8;
Indels 0;
Gaps 0;

OC
 OC
 Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 euroids I; Cucurbitales; Begoniaceae; Begonia.
 NEBI_TAXID=80370;
 [1]
 RP
 SEQUENCE FROM N A.
 Chiang T.Y.;
 "Sequence announcement: rbcL promoter gene in Begonia formosana.";
 Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 EMBL: AJ005957; CAB52119.1; -;
 Chloroplast.
 FT
 NON_TER 8
 SEQUENCE 8 AA: 921 MW: FA21AB01B6C77B6 CRC64:
 SQ

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: January 17, 2002, 12:12:40 ; Search time 23.54 Seconds
(without alignments)
25.174 Million cell updates/sec

Title: US-09-424-080a-1
perfect score: 42
Sequence: 1 LPEKKYSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Maximum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq 1101:*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
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- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
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- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	26	61.9	6 15	AAR59959
2	24	57.1	6 21	AAB26378
3	24	57.1	6 22	AAD0552
4	24	57.1	7 20	AAR9336
5	24	57.1	7 22	AAB61834
6	24	57.1	8 16	AAW21215
7	24	57.1	8 16	AAR36175
8	21	50.0	8 14	AAR36175
9	21	50.0	8 20	AYA08148
10	21	50.0	8 20	AYA08148
11	21	50.0	8 20	AYA08149

RESULT 1		ALIGNMENTS	
ID	AAK59959	standard; peptide;	6 AA.
AC	AAK59959;		
XX			
DT	14-FEB-1995 (first entry)		
DE	peptide signal sequence for treating leukocyte interferon diseases.		
XX			
KW	therapeutic; metabolic interactions; PSS; analogues.		
XX			
OS	Synthetic.		
XX			
PN	W09416328-A.		
XX			
PD	21-JUL-1994.		
XX			
PF	30-DEC-1993;		
XX			
PR	30-DEC-1992;		
XX			
PA	(RATH/) RATH M.		
XX			
PI	Rath M;		
XX			
DR	WPI: 1994-249399/30.		
XX			
PT	Identifying peptide signal sequences in a protein - and use of their synthetic analogues for treating or preventing, e.g. cardiovascular and auto-immune disease, infections and cancer.		
XX			
PT	cardiovascular		
PT	auto-immune disease		
PT	infections		
PT	and cancer.		
PS	Claim 29; Page 14; 28pp; English.		
XX			

Clotting factor VI
Human hepreceptor
Residues 314-320 o
Non-polio enterovi
Coxsackievirus A V
Insulin like growt
Human protein frag
Human protein frag
Heptapeptide M4.
Human insulin 1/112 split
Peptide #3 used to
PH60(c-src) kinase
HTV-1 pol peptide
SEQ ID No 438 from
Mouse polyoma mido
Marine TC-CSF ince
Peptide ligand bin
Human plasminogen
Urokinase-type plasminogen-activating enzyme
Recombinant timoth
Human Kringle 5 pe
Tyrosine phosphatid
SH2-binding peptid
Immunogenic peptid
Peptide Wif 88-95.
T cell epitope/MHC
Vir-derived HIV pr
Mouse immunoglobul

OM protein - protein search, using sw model
Run on: January 17, 2002, 12:14:15 ; Search time 12.51 Seconds
(without alignments)
14.391 Million cell updates/sec

Title: US-09-424-080a-1
Perfect score: 42
Sequence: 1 LTKKYSR 8
Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 212252 seqs, 22501292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Issued.Patents_AA:*
- 1: /cgn2_6/podata/2/1aa/5A,COMB.pep:*
- 2: /cgn2_6/podata/2/1aa/5A,COMB.pep:*
- 3: /cgn2_6/podata/2/1aa/5A,COMB.pep:*
- 4: /cgn2_6/podata/2/1aa/6B,COMB.pep:*
- 5: /cgn2_6/podata/2/1aa/backfiles1,pep:*
- 6: /cgn2_6/podata/2/1aa/backfiles1,pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	42	100.0	8	US-09-08-669-284B-30
2	42	61.9	6	US-09-08-669-284B-30
3	24	57.1	6	US-09-616-368A-15
4	24	57.1	6	US-09-054-298-15
5	24	57.1	6	US-08-818-655-15
6	24	57.1	7	US-08-891-271-13
7	22	52.4	7	US-08-756-849-123
8	21	50.0	8	US-08-444-118-659
9	20	47.6	7	US-08-390-453A-9
10	20	47.6	7	US-09-371-110-48
11	20	47.6	7	US-09-447-333-31
12	20	47.6	7	US-08-862-124-23
13	20	47.6	7	US-08-862-124-26
14	20	47.6	7	US-09-548-336-48
15	20	47.6	8	US-08-178-570-47
16	20	47.6	8	US-08-369-643-47
17	20	47.6	8	PCT-US95-0147-47
18	19	45.2	6	US-08-676-318-8
19	19	45.2	7	US-07-638-492-15
20	19	45.2	7	US-08-604-965E-10
21	19	45.2	7	US-08-178-570-47
22	19	45.2	8	US-08-178-570-48
23	19	45.2	8	US-08-369-643-48
24	19	45.2	8	PCT-US95-00147-48
25	19	45.2	8	PCT-US95-00147-48
26	19	45.2	8	525287-44
27	18	42.9	5	US-08-928-958-20

ALIGNMENTS

RESULT 1
US-08-669-284B-30
Sequence 30, Application US/08669284B
Patient No. 5939534
GENERAL INFORMATION:
APPLICANT: Inoue, Makoto
APPLICANT: Ito, Akira
APPLICANT: Kikuchi, Kaoru
APPLICANT: Ishire, Yoko
APPLICANT: Kimura, Toru
APPLICANT: Nakayama, Chikao
APPLICANT: No. 5939534
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGIRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669, 284B
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/02269
APPLICATION NUMBER: PCT/JP94/02269
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-268281
APPLICATION NUMBER: JP 05-350934
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-201504
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H
REGISTRATION NUMBER: 33, 981
REFERENCE/DOCKET NUMBER: Q-42041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)295-7060
TELEFAX: (202)295-7860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-669-284B-30

Query Match , 100.0%; Score 42; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 1 LTEKKYSP 8
 Db 1 LTEKKYSP 8

RESULT 2
 PCT-US93-12679-16

Sequence 16, Application PC/TUS9312679
 GENERAL INFORMATION:

APPLICANT: Rath, Matthias
 TITLE OF INVENTION: SYNTHETIC OLIGOBEPIDES ANALOGOUS TO PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND NUMBER OF SEQUENCES: 41

TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND

NUMBER OF SEQUENCES: 40

RESULT 3
 US-08-616-368A-15

Sequence 15, Application US/08616368A

Patent No. 5,767,262

GENERAL INFORMATION:

APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar
 APPLICANT: Jain, Mukesh
 APPLICANT: Yet, Shaw-Fang
 ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatientIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/616,368A
 FILING DATE: 15-MAR-1996
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATRY NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 05433/022001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-616-368A-15

Query Match , 57.1%; Score 24; DB 1; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.6e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;
 QY 4 KKYS 8
 Db 1 KKYS 5

RESULT 4
 US-09-054-298-15

Sequence 15, Application US/09054298
 Patent No. 6,136,953

GENERAL INFORMATION:
 APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar
 APPLICANT: Jain, Mukesh
 APPLICANT: Yet, Shaw-Fang

TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
 NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ For Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/054,298

US-08-818-655-15

FILING DATE: 02-APR-1998

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/616,368

FILING DATE: 15-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Beattie, Ph.D., Ingrid A.

REGISTRATION NUMBER: P-42,306

REFERENCE/DOCKET NUMBER: 05433/022002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

RESULT 6

US-08-891-271-13

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6165476

GENERAL INFORMATION:

APPLICANT: Strom, Terry B.

ATTORNEY: Sytkowski, Arthur J.

APPLICANT: Zheng, Xin Xiao

TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Milnitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patient Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/891,271

FILING DATE: 10-JUL-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hogle, Doreen M.

REGISTRATION NUMBER: 36,361

REFERENCE/DOCKET NUMBER: BIH97-07

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-891-271-13

Query Match 57.1%; Score 24; DB 4; Length 7;

Sequence 123, Application US/08756849

Patient No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 5

US-08-818-655-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 4

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 3

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 1

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;

Sequence 13, Application US/08891271

Best Local Similarity 80.0%; Pred. No. 1.6e+05; 0; Mismatches

Matches 4; Conservative 0; Indels 1; Gaps 0;

Patent No. 6093810

GENERAL INFORMATION:

APPLICANT: Bird, David MCK.

ATTORNEY: Wilson, Mark A.

TITLE OF INVENTION: Nematode-Induced Genes in Tomato

RESULT 0

NUMBER OF SEQUENCES:		129
CORRESPONDENCE ADDRESS:		
ADDRESS:		Townsend and Townsend and Crew LLP
STREET:		Two Embarcadero Center, Eighth Floor
CITY:		San Francisco
STATE:		California
COUNTRY:		USA
ZIP:		94111-3834
COMPUTER READABLE FORM:		
MEDIUM TYPE:		Floppy disk
COMPUTER:		IBM PC compatible
OPERATING SYSTEM:		PC-DOS/MS-DOS
SOFTWARE:		PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:		
APPLICATION NUMBER:		US/08/444,818
FILING DATE:		14-MAR-1995
CLASSIFICATION:		424
PRIORITY APPLICATION DATA:		
APPLICATION NUMBER:		US/08/403,590
FILING DATE:		25-MAY-1994
ATTORNEY/AGENT INFORMATION:		
NAME:		Bastian, Kevin L.
REGISTRATION NUMBER:		34,774
REFERENCE/DOCKET NUMBER:		023070-053510US
TELECOMMUNICATION INFORMATION:		
TELEPHONE:		(415) 576-0200
TELEFAX:		(415) 576-0300
SEQUENCE INFORMATION FOR SEQ ID NO:		123:
SEQUENCE CHARACTERISTICS:		
LENGTH:		7 amino acids
TYPE:		amino acid
STRANDEDNESS:		
TOPOLOGY:		linear
MOLECULE TYPE:		peptide
MOLECULE TYPE:		peptide
RESULT		9
Query Match		50.0%
Best Local Similarity		66.7%
Matches		4; Conservative
Qy		1 LTEKKY 6
Db		1 LITERLY 6
US-08-390-353A-9		
Sequence 9, Application US/08390353A		
Patent No. 6107457		
GENERAL INFORMATION:		
APPLICANT:		Arlinghaus, Ralph B.
APPLICANT:		Liu, Jiaxin
APPLICANT:		Lu, Dia
APPLICANT:		Lopez-Berestein, Gabriel
TITLE OF INVENTION:		Bcr-Ab1 Directed Compositions and Uses for Regulating Philadelphia Chromosome Stimulated Cell Activity
TITLE OF INVENTION:		Regulating Philadelphia Chromosome Stimulated Cell Activity
NUMBER OF SEQUENCES:		21
CORRESPONDENCE ADDRESS:		
ADDRESSEE:		Arnold, White & Durkee
STREET:		P. O. Box 4433
CITY:		Houston
STATE:		Texas
COUNTRY:		US
ZIP:		77210
COMPUTER READABLE FORM:		
MEDIUM TYPE:		Floppy disk
COMPUTER:		IBM PC compatible
OPERATING SYSTEM:		PC-DOS/MS-DOS
SOFTWARE:		PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:		
APPLICATION NUMBER:		US/08/390,353A
FILING DATE:		16-FEB-1995
CLASSIFICATION:		514
ATTORNEY/AGENT INFORMATION:		
NAME:		Mayfield, Denise L.
REGISTRATION NUMBER:		33,732
REFERENCE/DOCKET NUMBER:		US/SC:421/MAY
TELECOMMUNICATION INFORMATION:		
TELEPHONE:		(512) 418-3000
TELEFAX:		(512) 474-7577
TELEFAX:		N/A
INFORMATION FOR SEQ ID NO:		9:
SEQUENCE CHARACTERISTICS:		
LENGTH:		7 amino acids
TYPE:		amino acid
STRANDEDNESS:		single
TOPOLOGY:		linear
MOLECULE TYPE:		peptide
MOLECULE TYPE:		peptide
US-08-390-353A-9		

us-09-424-080a-1.closed.rail

Query Match 47.6%; Score 20; DB 3'; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.6e+05; 1; Mismatches
 Matches 3; Conservative 1; Indels 0; Gaps 0;

Qy 4 KRYSP 8
 Db 1 PSYSP 5

RESULT 10
 US-09-371-710-4B
 Sequence 4B, Application US/09371710A
 Patent No. 614866
 GENERAL INFORMATION:
 APPLICANT: Korel, Thomas R.
 APPLICANT: Bloomer, Sherri L.
 APPLICANT: Savoy, Anne C.
 TITLE OF INVENTION: GlycurooxyLmannan (GXM)-O-AcetylHydrolase of
 TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
 FILE REFERENCE: D6245
 CURRENT APPLICATION NUMBER: US/09/371.710A
 CURRENT FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 50
 SEQ ID NO 4B
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer
 US-09-371-710-4B

RESULT 11
 US-09-147-933-31
 Query Match 47.6%; Score 20; DB 4'; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05; 1; Mismatches
 Matches 3; Conservative 1; Indels 0; Gaps 0;
 Qy 5 KYSP 8
 Db 2 KYAP 5

Query Match 47.6%; Score 20; DB 4'; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05; 1; Mismatches
 Matches 3; Conservative 1; Indels 0; Gaps 0;
 Qy 5 KYSP 8
 Db 2 KYAP 5

RESULT 11
 US-09-147-933-31
 Sequence 31, Application US/09147933A
 Patent No. 6168917
 GENERAL INFORMATION:
 APPLICANT: Kilpatrick, David
 APPLICANT: Kilpatrick, David
 TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
 TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES
 FILE REFERENCE: 62242.US
 CURRENT APPLICATION NUMBER: US/09/147.933A
 CURRENT FILING DATE: 1999-07-09
 EARLIER APPLICATION NUMBER: PCT/US97/17734
 EARLIER FILING DATE: 1997-10-01
 EARLIER APPLICATION NUMBER: U. S. 60/027,353
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 31
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: peptide
 US-09-147-933-31

RESULT 12
 US-08-862-124-23
 Sequence 23, Application US/08862124
 Patent No. 6207153
 GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 APPLICANT: Maiti, Pradip K.
 APPLICANT: Kaplan, Howard A.
 APPLICANT: Kaplan, Howard A.
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
 TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
 TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
 TITLE OF INVENTION: DETECTION OF CANCERS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster LLP
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/862.124
 FILING DATE: 22-MAY-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001-20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEX: 706141
 FAX: (650) 494-0792
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-862-124-23

RESULT 13
 US-08-862-124-26
 Sequence 26, Application US/08862124
 Patent No. 6207153
 GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 APPLICANT: Maiti, Pradip K.
 APPLICANT: Kaplan, Howard A.
 APPLICANT: Kaplan, Howard A.
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
 TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
 TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
 TITLE OF INVENTION: DETECTION OF CANCERS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.30

APPLICATION NUMBER: US/08/862,124
 FILING DATE: 22 MAY 1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Lehhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein

US-08-862-124-26

Query Match 47.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.6e+05; Mismatches 3; Conservative 1; Indels 0; Gaps 0;

Qy 5 KYSP 8
 Db 3 RYSP 6

RESULT 14
 US-09-648-386-48
 Sequence 48, Application US/09648386
 Patent No. 6284508
 GENERAL INFORMATION:
 APPLICANT: Bloomer, Sherri L.
 APPLICANT: Savoy, Anne C.
 TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of Cryptococcus neoformans and Uses Thereof
 FILE REFERENCE: D6245D
 CURRENT APPLICATION NUMBER: US/09/648 386
 CURRENT FILING DATE: 2000-08-25
 PRIOR APPLICATION NUMBER: US 09/371,710
 PRIOR FILING DATE: 1999-08-09
 NUMBER OF SEQ ID NOS: 50
 SEQ ID NO 48
 LENGTH: 7
 TYPE: PRY
 FEATURE: Artificial sequence
 ORGANISM: Associated amino acid sequence of PCR primer 34-mer

us-09-648-386-48

Query Match 47.6%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+05; Mismatches 3; Conservative 2; Indels 0; Gaps 0;

Qy 3 EKYSP 8
 Db 1 EEBYMP 6

Search completed: January 17, 2002, 12:16:07
 Job time: 112 sec